OIPE

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/085,188

DATE: 03/19/2002
TIME: 15:53:43

Input Set : A:\98-69C1.SEQ.txt
Output Set: N:\CRF3\03192002\J085188.raw

```
     4  <110>  APPLICANT: Presnell, Scott R.
     5         Taft, David W.
     7  <120>  TITLE OF INVENTION: A New Member of the Human
     8         Syntaxin/Epimorphin Family
    10  <130>  FILE REFERENCE: 98-69
C--> 12  <140>  CURRENT APPLICATION NUMBER: US/10/085,188
C--> 12  <141>  CURRENT FILING DATE: 2002-02-26
    12  <160>  NUMBER OF SEQ ID NOS: 9
    14  <170>  SOFTWARE: FastSEQ for Windows Version 3.0
    16  <210>  SEQ ID NO: 1
    17  <211>  LENGTH: 1274
    18  <212>  TYPE: DNA
    19  <213>  ORGANISM: Homo sapiens
    21  <220>  FEATURE:
    22  <221>  NAME/KEY: CDS
    23  <222>  LOCATION: (189)...(1049)
    25  <400>  SEQUENCE: 1
    26   gcggccgcgg cggcgcggag ctcgggcggc cgtggaggaa ctcagcctcg gccgcaggag      60
    27   gcgccgggag cggagccgcc gggagtcgcg caacaggttt ccttctccat cgctgcgccc     120
    28   acaggggacg cgcgccctgc cgggagaggg gcttctcggt tcgcactctc gctcccagtc     180
    29   caggcaaa atg aaa gac cgg cta gca gaa ctt ctg gac ttg tcc aag caa      230
    30           Met Lys Asp Arg Leu Ala Glu Leu Leu Asp Leu Ser Lys Gln
    31             1               5                   10
    33   tat gac cag cag ttc cca gac ggg gac gat gag ttt gac tcg ccc cac      278
    34   Tyr Asp Gln Gln Phe Pro Asp Gly Asp Asp Glu Phe Asp Ser Pro His
    35    15               20                25                  30
    37   gag gac atc gtg ttc gag acg gac cac atc ctg gag tcc ctg tac cga      326
    38   Glu Asp Ile Val Phe Glu Thr Asp His Ile Leu Glu Ser Leu Tyr Arg
    39                    35                40                  45
    41   gac atc cgg gac att cag gat gaa aac cag ctg ctg gtg gcc gac gtg      374
    42   Asp Ile Arg Asp Ile Gln Asp Glu Asn Gln Leu Leu Val Ala Asp Val
    43                    50                55                  60
    45   aag cgg ctg gga aag cag aac gcc cgc ttc ctc acg tcc atg cgg cgc      422
    46   Lys Arg Leu Gly Lys Gln Asn Ala Arg Phe Leu Thr Ser Met Arg Arg
    47             65                70                  75
    49   ctc agc agc atc aag cgc gac acc aac tcc atc gcc aag gcc atc aag      470
    50   Leu Ser Ser Ile Lys Arg Asp Thr Asn Ser Ile Ala Lys Ala Ile Lys
    51          80                85                  90
    53   gcc cgg ggc gag gtc atc cac tgc aag ctg cgc gcc atg aag gag ctg      518
    54   Ala Arg Gly Glu Val Ile His Cys Lys Leu Arg Ala Met Lys Glu Leu
    55    95              100                 105                 110
    57   agc gag gcg gct gag gcc cag cac ggc ccg cac tcg gca gtg gcg cgc      566
    58   Ser Glu Ala Ala Glu Ala Gln His Gly Pro His Ser Ala Val Ala Arg
```

```
59                115               120               125
61  att tcg cgg gcg cag tac aac gcg ctc acc ctc acc ttc cag cgc gcc    614
62  Ile Ser Arg Ala Gln Tyr Asn Ala Leu Thr Leu Thr Phe Gln Arg Ala
63                130               135               140
65  atg cac gac tac aac cag gcc gag atg aag cag cgc gac aac tgc aag    662
66  Met His Asp Tyr Asn Gln Ala Glu Met Lys Gln Arg Asp Asn Cys Lys
67                145               150               155
69  atc cgc atc cag cgc cag ctg gag atc atg ggc aag gaa gtc tcg ggc    710
70  Ile Arg Ile Gln Arg Gln Leu Glu Ile Met Gly Lys Glu Val Ser Gly
71            160               165               170
73  gac cag atc gag gac atg ttc gag cag ggt aag tgg gac gtg ttt tcc    758
74  Asp Gln Ile Glu Asp Met Phe Glu Gln Gly Lys Trp Asp Val Phe Ser
75  175               180               185               190
77  gag aac ttg ctg gcc gac gtg aag ggc gcg cgg gcc gcc ctc aac gag    806
78  Glu Asn Leu Leu Ala Asp Val Lys Gly Ala Arg Ala Ala Leu Asn Glu
79                195               200               205
81  atc gag agc cgc cac cgc gaa ctg ctg cgc ctg gag agc cgc atc cgc    854
82  Ile Glu Ser Arg His Arg Glu Leu Leu Arg Leu Glu Ser Arg Ile Arg
83                210               215               220
85  gac gta cac gag ctc ttc ttg cag atg gcg gtg ctg gtg gag aag cag    902
86  Asp Val His Glu Leu Phe Leu Gln Met Ala Val Leu Val Glu Lys Gln
87            225               230               235
89  gcc gac acc ctg aac gtc atc gag ctc aac gta caa aag acg gtc gac    950
91  Ala Asp Thr Leu Asn Val Ile Glu Leu Asn Val Gln Lys Thr Val Asp
92            240               245               250
94  tac acc ggc cag gcc aag gcg cag gtg cgg aag gcc gtg cag tac gag    998
95  Tyr Thr Gly Gln Ala Lys Ala Gln Val Arg Lys Ala Val Gln Tyr Glu
96  255               260               265               270
98  gag aag aac ccc tgc cgg acc ctc tgc tgc ttc tgc tgt ccc tgc ctc   1046
99  Glu Lys Asn Pro Cys Arg Thr Leu Cys Cys Phe Cys Cys Pro Cys Leu
100               275               280               285
102  aag tagcaggccg gcccgggccg ccaccgccca tcccagacca tggagcgcgc        1099
103  tgggaaggac gcaccaaagc cgggagctct gccctgcagg gagttgcccc aacccttttcc 1159
104  ggaactcagt ctttagaaaa gaaacgccag gttcaagaat tgcaaaccag cctgtgcttg  1219
105  gaaagatggt tagttgatac cgtccgatga ttcttcagta aagatagatt cccac        1274
107  <210> SEQ ID NO: 2
108  <211> LENGTH: 287
109  <212> TYPE: PRT
110  <213> ORGANISM: Homo sapiens
112  <400> SEQUENCE: 2
113  Met Lys Asp Arg Leu Ala Glu Leu Leu Asp Leu Ser Lys Gln Tyr Asp
114   1               5                10                15
115  Gln Gln Phe Pro Asp Gly Asp Asp Glu Phe Asp Ser Pro His Glu Asp
116            20                25                30
117  Ile Val Phe Glu Thr Asp His Ile Leu Glu Ser Leu Tyr Arg Asp Ile
118            35   .            40                45
119  Arg Asp Ile Gln Asp Glu Asn Gln Leu Leu Val Ala Asp Val Lys Arg
120       50                55                60
121  Leu Gly Lys Gln Asn Ala Arg Phe Leu Thr Ser Met Arg Arg Leu Ser
```

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                 RAW SEQUENCE LISTING              DATE: 03/19/2002
                 PATENT APPLICATION:  US/10/085,188  TIME: 15:53:43

                 Input Set : A:\98-69C1.SEQ.txt
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```

```
122  65                    70                  75                  80
123  Ser Ile Lys Arg Asp Thr Asn Ser Ile Ala Lys Ala Ile Lys Ala Arg
124                  85                  90                  95
125  Gly Glu Val Ile His Cys Lys Leu Arg Ala Met Lys Glu Leu Ser Glu
126                  100                 105                 110
127  Ala Ala Glu Ala Gln His Gly Pro His Ser Ala Val Ala Arg Ile Ser
128                  115                 120                 125
129  Arg Ala Gln Tyr Asn Ala Leu Thr Leu Thr Phe Gln Arg Ala Met His
130             130                 135                 140
131  Asp Tyr Asn Gln Ala Glu Met Lys Gln Arg Asp Asn Cys Lys Ile Arg
132  145                 150                 155                 160
133  Ile Gln Arg Gln Leu Glu Ile Met Gly Lys Glu Val Ser Gly Asp Gln
134                  165                 170                 175
136  Ile Glu Asp Met Phe Glu Gln Gly Lys Trp Asp Val Phe Ser Glu Asn
137                  180                 185                 190
138  Leu Leu Ala Asp Val Lys Gly Ala Arg Ala Ala Leu Asn Glu Ile Glu
139             195                 200                 205
140  Ser Arg His Arg Glu Leu Leu Arg Leu Glu Ser Arg Ile Arg Asp Val
141  210                 215                 220
142  His Glu Leu Phe Leu Gln Met Ala Val Leu Val Glu Lys Gln Ala Asp
143  225                 230                 235                 240
144  Thr Leu Asn Val Ile Glu Leu Asn Val Gln Lys Thr Val Asp Tyr Thr
145                  245                 250                 255
146  Gly Gln Ala Lys Ala Gln Val Arg Lys Ala Val Gln Tyr Glu Glu Lys
147             260                 265                 270
148  Asn Pro Cys Arg Thr Leu Cys Cys Phe Cys Cys Pro Cys Leu Lys
149             275                 280                 285
151  <210> SEQ ID NO: 3
152  <211> LENGTH: 861
153  <212> TYPE: DNA
154  <213> ORGANISM: Artificial Sequence
156  <220> FEATURE:
157  <223> OTHER INFORMATION: This degenerate sequence encodes the amino acid
158        sequence of SEQ ID NO:2.
160  <221> NAME/KEY: variation
161  <222> LOCATION: (1)...(861)
162  <223> OTHER INFORMATION: N is any nucleotide.
164  <400> SEQUENCE: 3
```

```
W--> 165  atgaargaym gnytngcnga rytnytngay ytnwsnaarc artaygayca rcarttyccn   60
W--> 166  gayggngayg aygarttyga ywsnccncay gargayathg tnttygarac ngaycayath  120
W--> 167  ytngarwsny tntaymgnga yathmgngay athcargayg araaycaryt nytngtngcn  180
W--> 168  gaygtnaarm gnytnggnaa rcaraaygcn mgnttyytna cnwsnatgmg nmgnytnwsn  240
W--> 169  wsnathaarm gngayacnaa ywsnathgcn aargcnatha argcnmgngg ngargtnath  300
W--> 170  caytgyaary tnmgngcnat gaargarytn wsngargcng cngargcnca rcayggnccn  360
W--> 171  caywsngcng tngcnmgnat hwsnmgngcn cartayaayg cnytnacnyt nacnttycar  420
W--> 172  mgngcnatgc aygaytayaa ycargcngar atgaarcarm gngayaaytg yaarathmgn  480
W--> 173  athcarmgnc arytngarat hatgggnaar gargtnwsng gngaycarat hgargayatg  540
W--> 174  ttygarcarg gnaartggga ygtnttywsn garaayytny tngcngaygt naarggngcn  600
W--> 175  mgngcngcny tnaaygarat hgarwsnmgn caymgngary tnytnmgnyt ngarwsnmgn  660
```

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```
W--> 176  athmgngayg tncaygaryt nttyytncar atggcngtny tngtngaraa rcargcngay     720
W--> 177  acnytnaayg tnathgaryt naaygtncar aaracngtng aytayacngg ncargcnaar     780
W--> 178  gcncargtnm gnaargcngt ncartaygar garaaraayc cntgymgnac nytntgytgy     840
W--> 179  ttytgytgyc cntgyytnaa r                                               861
     181  <210> SEQ ID NO: 4
     182  <211> LENGTH: 18
     183  <212> TYPE: DNA
     184  <213> ORGANISM: Artificial Sequence
     186  <220> FEATURE:
     187  <223> OTHER INFORMATION: PCR primer
     189  <400> SEQUENCE: 4
     190   tggcggtgct ggtggaga                                                   18
     192  <210> SEQ ID NO: 5
     193  <211> LENGTH: 18
     194  <212> TYPE: DNA
     195  <213> ORGANISM: Artificial Sequence
     197  <220> FEATURE:
     198  <223> OTHER INFORMATION: PCR primer
     200  <400> SEQUENCE: 5
     201   ccggcagggg ttcttctc                                                  18
     203  <210> SEQ ID NO: 6
     204  <211> LENGTH: 287
     205  <212> TYPE: PRT
     206  <213> ORGANISM: Homo sapiens
     208  <400> SEQUENCE: 6
     209   Met Lys Asp Arg Leu Ala Glu Leu Leu Asp Leu Ser Lys Gln Tyr Asp
     210    1               5                  10                  15
     211   Gln Gln Phe Pro Asp Gly Asp Asp Glu Phe Asp Ser Pro His Glu Asp
     212                  20                  25                  30
     213   Ile Val Phe Glu Thr Asp His Ile Leu Glu Ser Leu Tyr Arg Asp Ile
     214              35                  40                  45
     215   Arg Asp Ile Gln Asp Glu Asn Gln Leu Leu Val Ala Asn Val Lys Arg
     216        50                  55                  60
     217   Leu Gly Lys Gln Asn Ala Arg Phe Leu Thr Ser Met Arg Arg Leu Ser
     218   65                  70                  75                  80
     219   Ser Ile Lys Arg Asp Thr Asn Ser Ile Ala Lys Ala Ile Lys Ala Pro
     220                  85                  90                  95
     221   Pro Glu Val Ile His Cys Asn Val Arg Ala Met Lys Glu Leu Ser Glu
     222                  100                 105                 110
     223   Ala Ala Glu Ala Gln His Gly Pro Ala Leu Gly Ser Gly Gly Ile Ser
     224              115                 120                 125
     226   Arg Ala Gln Tyr Asn Ala Leu Thr Leu Thr Phe Gln Arg Ala Met His
     227        130                 135                 140
     228   Asp Tyr Asn Gln Ala Glu Met Lys Gln Arg Asp Asn Cys Lys Ile Arg
     229   145                 150                 155                 160
     230   Ile Gln Arg Gln Leu Glu Ile Met Gly Lys Glu Val Ser Gly Asp Gln
     231                  165                 170                 175
     232   Ile Glu Asp Met Phe Glu Gln Gly Lys Trp Asp Val Phe Ser Glu Asn
     233                  180                 185                 190
```

RAW SEQUENCE LISTING   DATE: 03/19/2002
PATENT APPLICATION: US/10/085,188   TIME: 15:53:43

Input Set : A:\98-69C1.SEQ.txt
Output Set: N:\CRF3\03192002\J085188.raw

```
234  Leu Leu Ala Asp Val Lys Gly Val Arg Ala Ala Leu Asn Glu Ile Glu
235          195             200             205
236  Ser Arg His Arg Glu Leu Val Arg Leu Glu Ser Ala Ile Arg Asp Val
237      210             215             ·    220
238  His Glu Leu Phe Leu Gln Met Ala Val Leu Val Glu Lys Gln Ala Asp
239  225             230             235             240
240  Thr Leu Asn Val Ile Glu Leu Asn Val Gln Lys Thr Val Asp Tyr Thr
241              245             250             255
242  Gly Gln Ala Lys Ala Gln Val Arg Lys Ala Val Gln Tyr Glu Glu Lys
243          260             265             270
244  Asn Pro Cys Arg Thr Leu Cys Cys Phe Cys Cys Pro Cys Leu Lys
245          275             280             285
247  <210> SEQ ID NO: 7
248  <211> LENGTH: 22
249  <212> TYPE: DNA
250  <213> ORGANISM: Artificial Sequence
252  <220> FEATURE:
253  <223> OTHER INFORMATION: PCR primer
255  <400> SEQUENCE: 7
256   ggacgtgttt tccgagaact tg                                          22
258  <210> SEQ ID NO: 8
259  <211> LENGTH: 22
260  <212> TYPE: DNA
261  <213> ORGANISM: Artificial Sequence
263  <220> FEATURE:
264  <223> OTHER INFORMATION: PCR primer
266  <400> SEQUENCE: 8
267   cgaccgtctt ttgtacgttg ag                                          22
269  <210> SEQ ID NO: 9
270  <211> LENGTH: 16
271  <212> TYPE: PRT
272  <213> ORGANISM: Artificial Sequence
274  <220> FEATURE:
275  <223> OTHER INFORMATION: Peptide linker.
277  <400> SEQUENCE: 9
278   Gly Gly Ser Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
279   1               5               10              15
```

VERIFICATION SUMMARY   DATE: 03/19/2002
PATENT APPLICATION: **US/10/085,188**   TIME: 15:53:44

Input Set : **A:\98-69Cl.SEQ.txt**
Output Set: **N:\CRF3\03192002\J085188.raw**

```
L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:170 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:171 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:173 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:175 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:177 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
```